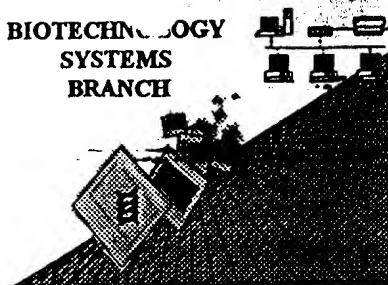


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/658,835

Source: OIPE

Date Processed by STIC: 9-22-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/658,835

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

Protestant Church
Community Development

6,

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/658,835

DATE: 09/22/2000

TIME: 14:59:33

Input Set : A:\1134RSEQLIST.TXT

Output Set: N:\CRF3\09222000\I658835.raw

```

64 -211- LENGTH: 29
65 -212- TYPE: DNA
66 -213- ORGANISM: Artificial Sequence
67 -220- FEATURE:
68 -221- OTHER INFORMATION: Designed oligonucleotide for 3' RACE. N21965
69 -100- SEQUENCE: 3
70 -100- SEQUENCE: 3
71 -210- SEQ ID NO: 1
72 -211- LENGTH: 28
73 -212- TYPE: DNA
74 -213- ORGANISM: Artificial Sequence
75 -220- FEATURE:
76 -221- OTHER INFORMATION: Designed oligonucleotide for 3' RACE. 21968
77 -100- SEQUENCE: 1
78 -100- SEQUENCE: 1
79 -210- SEQ ID NO: 5
80 -211- LENGTH: 1389
81 -212- TYPE: DNA
82 -213- ORGANISM: Exophiala spinifera
83 -220- FEATURE:
84 -221- NAME/KEY: CDS
85 -222- LOCATION: (1)...(1386)
86 -100- SEQUENCE: 5
87 -100- SEQUENCE: 5
88 -100- SEQUENCE: 5
89 -100- SEQUENCE: 5
90 -100- SEQUENCE: 5
91 -100- SEQUENCE: 5
92 -100- SEQUENCE: 5
93 -100- SEQUENCE: 5
94 -100- SEQUENCE: 5
95 -100- SEQUENCE: 5
96 -100- SEQUENCE: 5
97 -100- SEQUENCE: 5
98 -100- SEQUENCE: 5
99 -100- SEQUENCE: 5
100 -100- SEQUENCE: 5
101 -100- SEQUENCE: 5
102 -100- SEQUENCE: 5
103 -100- SEQUENCE: 5
104 -100- SEQUENCE: 5
105 -100- SEQUENCE: 5
106 -100- SEQUENCE: 5
107 -100- SEQUENCE: 5
108 -100- SEQUENCE: 5
109 -100- SEQUENCE: 5
110 -100- SEQUENCE: 5
111 -100- SEQUENCE: 5
112 -100- SEQUENCE: 5
113 -100- SEQUENCE: 5
114 -100- SEQUENCE: 5
115 -100- SEQUENCE: 5
116 -100- SEQUENCE: 5
117 -100- SEQUENCE: 5
118 -100- SEQUENCE: 5
119 -100- SEQUENCE: 5
120 -100- SEQUENCE: 5
121 -100- SEQUENCE: 5
122 -100- SEQUENCE: 5
123 -100- SEQUENCE: 5
124 -100- SEQUENCE: 5
125 -100- SEQUENCE: 5
126 -100- SEQUENCE: 5
127 -100- SEQUENCE: 5
128 -100- SEQUENCE: 5
129 -100- SEQUENCE: 5

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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/658,835

DATE: 09/22/2000

TIME: 11:59:33

Input Set: A:\1134RSEQLIST.TXT

Output Set: N:\CRF3\09222000\I658835.raw

130	130	135	140	
131	ctc gac agt gtt agc ttc ggc cac tac tgt gag aag gaa cta aac ttg	180		
132	Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu			
133	145	150	155	160
134	ccg gct gtt ctc ggc gta gca aac cac atc aca cgc gct cta ctc ggt	628		
135	Pro Ala Val Leu Cys Val Ala Asn Cln Ile Thr Arg Ala Leu Leu Gly			
136	175	180	185	190
137	gtg gaa gcc cac aac atc acc atg att ttt ctc acc gac tac atc aag	676		
138	Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys			
139	195	200	205	210
140	agt gcc acc ggt ctc agt aat att ttc tgg cac aag aaa gac ggc ggc	621		
141	Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly			
142	215	220	225	230
143	cag tat atg cga tgc aaa agt ggt atc gag tgg att tgc cat gac atg	672		
144	Gln Tyr Met Asn Cln Lys Thr Gly Met Gln Ser Ile Cys His Ala Met			
145	235	240	245	250
146	aca aag gaa ctt gtt cca ggc tgc gta cac ctc aac acc ccc gtc gct	720		
147	Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala			
148	255	260	265	270
149	gaa att aag cac tgc gca tgc ggc tgt aca gta cga tgg gcc tgg ggc	768		
150	Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly			
151	275	280	285	290
152	gcc gtg ttc cga aac aaa aat gta ctc gtt tgg tta ccc aca acc ttg	816		
153	Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu			
154	295	300	305	310
155	tat ccc acc ttg aca ttt tca cca cct ttt ccc gcc aag aag aca gca	864		
156	Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala			
157	315	320	325	330
158	ttg ggc gaa aat tct atc ctc ggc tac tat agc aag ata gtc ttc gta	912		
159	Leu Ala Gln Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val			
160	335	340	345	350
161	tgg gac aag cgg tgg tgg cgt gaa caa ggc ttc tgg ggc gtc ctc caa	960		
162	Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln			
163	355	360	365	370
164	tgg agc tgt gac ccc atc tca ttt gcc agt gat acc agc atc gac gtc	1008		
165	Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val			
166	375	380	385	390
167	gat cga caa tgg ttc att acc tgt ttc atg gtc gga gac ccc gga cgg	1056		
168	Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg			
169	395	400	405	410
170	aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac	1104		
171	Lys Trp Ser Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp			
172	415	420	425	430
173	caa ctc cgc gca gcc tac gag aac gcc ggc gcc caa gtc cca gag cgg	1152		
174	Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro			
175	435	440	445	450
176	gcc aac gtg ctc gaa atc gag tgg tgg aag gag cag tat ttc caa gga	1200		
177	Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly			
178	385	390	395	400

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/658,835

DATE: 09/22/2000

TIME: 11:59:33

Input Set : A:\1134RSEQLIST.TXT

Output Set : N:\CRF3\09222000\I658835.raw

```

196  gat cag agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcc 1218
197  Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
198  405 410 415
200  ggg ctg aga acc ccc ttc aag agt gtt cat ttc att aga acc aag agc 1296
201  Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
202  420 425 430
204  tct tta gtt tgg aac ggg tat atg gaa ggg acc ata cga tcc ggt caa 1344
205  Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
206  435 440 445
208  cga ggt gct gca gaa gtt gtg gct acc ctg gtg cca gca gca 1386
209  Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
210  450 455 460
212  tag 1489
213  210 - SEQ ID NO: 6
214  211 - LENGTH: 462
215  212 - TYPE: PRT
216  213 - ORGANISM: Exophiala spinitera
217  210 - SEQUENCE: 6
220  Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
221  1 5 10 15
222  Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
223  20 25 30
224  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
225  35 40 45
226  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
227  50 55 60
228  Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
229  65 70 75 80
230  Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
231  85 90 95
232  Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
233  100 105 110
234  Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
235  115 120 125
236  Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
237  130 135 140
238  Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
239  145 150 155 160
240  Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
241  165 170 175
242  Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
243  180 185 190
244  Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
245  195 200 205
246  Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
247  210 215 220
248  Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
249  225 230 235 240
250  Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly

```

RAW SEQUENCE LISTING

DATE: 09/22/2000

PATENT APPLICATION: US/09/658,835

TIME: 11:39:33

Input Set : A:\1134RSEQLIST.TXT

Output Set: N:\CRF3\09222000\I658835.raw

```

251                               245                               250                               255
252 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
253                               260                               265                               270
254 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
255                               275                               280                               285
256 Leu Ala Glu Asn Ser Ile Leu Glu Tyr Tyr Ser Lys Ile Val Phe Val
257                               290                               295                               300
258 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
259                               305                               310                               315
260 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
261                               320                               325                               330
262 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
263                               335                               340                               345
264 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
265                               350                               355                               360
266 Gln Leu Arg Ala Ala Tyr Gln Asn Ala Gly Ala Gln Val Pro Glu Pro
267                               365                               370                               375
268 Ala Asn Val Ile Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
269                               380                               385                               390
270 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
271                               395                               400                               405
272 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Gln Thr
273                               410                               415                               420
274 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
275                               425                               430                               435
276 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
277                               440                               445                               450
278 <10> SEQ ID NO: 7
279 <11> LENGTH: 1442
280 <12> TYPE: DNA
281 <13> ORGANISM: Exophiala spinifera
282 <14> FEATURE
283 <15> NAME/KEY: CDS
284 <16> LOCATION: (1)...(515)
285 <17> NAME/KEY: intron
286 <18> LOCATION: (517)...(599)
287 <19> NAME/KEY: CDS
288 <20> LOCATION: (700)...(1439)
289 <400> SEQUENCE: 7
290 gac aac gtt acg gac gtg gta gta gta ggc gct ggc ttg agc ggt ttg 48
291 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
292 1 5 10 15
293 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
294 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
295 20 25 30
296 gag gcg atg cat cgt gta gga gga aag act ctg agc gta caa tcg ggt 144
297 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
298 35 40 45
299 ccc gcc agg acg act atc aac gac ctc gcc gct gcg tgg atc aat gac 192

```

09/658, 835

P. 6

<210> 19 Seq # 14

<211> 692

<212> PRT

<213> Unknown

M. was made to, <210> to <213>

→ Addition to caption unknown

<400> 19

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
1				5				10						15	
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
			20					25					30		
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
			35				40					45			
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
			50			55					60				
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65					70					75				80	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
				85					90					95	

Sequence 19

12 on 19

Summary Sheet.

(Entire sequence not shown)



This error was
also indicated in
Sequence numbers:
21, 25, 27, 29, 31, and
33. Please review
and correct.

09/658, 835

P 7

<210> 20 Seq # 20
<211> 1464
<212> DNA
<213> Unknown

<220>
<223> Nucleotide sequence of K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize. Nucleotides 1-72, barley alpha amylase signal sequence, nucleotides 73-75, added lysine residue; nucleotides 76 -1464 , trAPAO cDNA.



For the sequence rules, <223> feature is allowed a maximum number of 4 lines, 72 spaces per line. This error is also indicated in sequence # 30.

F.Y.I. ↓

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 09/22/2000

PATENT APPLICATION: US/09/658,835

TIME: 14:59:31

Input Set : A:\1134RSEQLIST.TXT

Output Set: N:\CRF3\09222000\I658835.raw

L:17 M:270 C: Current Application Number differs. Replaced Current Application No
L:17 M:271 C: Current Filing Date differs. Replaced Current Filing Date
L:49 M:341 W: (16) "n" or "Xaa" used, for SEQ ID#:1
L:248 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 2
L:252 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 2
L:1237 M:255 W: Mandatory Feature missing. <220> FEATURE:
L:1242 M:255 W: Mandatory Feature missing. <223> OTHER INFORMATION:
L:1337 M:255 W: Field exceeds allowed number of lines. <223> Other Information:
L:1338 M:255 W: Field exceeds allowed number of lines. <223> Other Information:
L:1191 M:255 W: Mandatory Feature missing. <223> OTHER INFORMATION:
L:1098 M:255 W: Mandatory Feature missing. <223> OTHER INFORMATION:
L:1520 M:255 W: Mandatory Feature missing. <223> OTHER INFORMATION:
L:1992 M:255 W: Mandatory Feature missing. <220> FEATURE:
L:1992 M:255 W: Mandatory Feature missing. <223> OTHER INFORMATION:
L:156 M:255 W: Field exceeds allowed number of lines. <223> Other Information:
L:157 M:255 W: Field exceeds allowed number of lines. <223> Other Information:
L:1490 M:255 W: Mandatory Feature missing. <220> FEATURE:
L:1490 M:255 W: Mandatory Feature missing. <223> OTHER INFORMATION:
L:1818 M:255 W: Mandatory Feature missing. <220> FEATURE:
L:1818 M:255 W: Mandatory Feature missing. <223> OTHER INFORMATION:
L:1189 M:341 W: (16) "n" or "Xaa" used, for SEQ ID#:39
L:1250 M:341 W: (16) "n" or "Xaa" used, for SEQ ID#:10